

SEQUENCE LISTING

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NAGAI, KAZUO



<120> A GENE CODING FOR PENICILLIN BINDING PROTEIN AND A METHOD FOR PRODUCING L-GLUTAMIC ACID

<130> 196811US0PCT

<140> 09/623,596

<141> 2000-09-05

<150> PCT/JP99/01084

<151> 1999-03-05

<150> JP10-55608

<151> 1998-03-06

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<170> PatentIn version 3.0

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Met Ala Asn Thr Asp Thr Ile Asn Pro Asn Glu Asp Thr Gly Lys Gln
305 310 315 320

Ile Glu Gln Gly Lys Ser Phe Asp Asn Pro Ser Val Thr His Pro Phe
325 330 335

Glu Pro Gly Ser Val Ala Lys Val Ile Thr Ala Ala Gly Val Ile Gln
340 345 350

Asp Gly Leu Thr Thr Pro Asp Glu Val Leu Gln Val Pro Gly Ser Ile
355 360 365

Glu Met Ala Gly Val Ser Val Gly Asp Ala Trp Asp His Gly Val Val
370 375 380

Pro Tyr Thr Thr Ala Gly Ile Phe Gly Lys Ser Ser Asn Val Gly Thr
385 390 395 400

Leu Met Leu Ala His Gly Leu Gly Glu Asp Lys Phe Ala Asp Tyr Leu
405 410 415

Glu Arg Phe Gly Val Gly Gln Ser Thr Gly Ile Glu Leu Pro Ser Glu
420 425 430

Ser Gln Gly Leu Leu Pro Ala Arg Glu Gln Trp Ser Gly Gly Thr Phe
435 440 445

Ala Asn Leu Pro Ile Gly Gln Gly Met Ser Ile Thr Thr Leu Gln Met
450 455 460

Ala Gly Ile Tyr Gln Ala Leu Ala Asn Asp Gly Glu Arg Ile Glu Pro
465 470 475 480

Arg Ile Ile Lys Ser Val Thr Asp Ser Asp Gly Thr Val Leu Glu Gln
485 490 495

Pro Glu Pro Asp Lys Ile Gln Val Val Ser Ala Glu Ala Ala Arg Thr
500 505 510

Thr Val Asp Met Phe Arg Ser Val Thr Gln Val Asp Pro Leu Gly Val
515 520 525

His Lys Val Pro Leu Gln Thr Pro Pro Leu Arg Val Ile Lys Ser Gln
530 535 540

Val Arg Gln Val Arg Arg Lys Lys Leu Thr Pro Thr Arg Ala Arg Thr
545 550 555 560

Leu Thr Arg Asn Thr Gly Leu Pro Ser Arg Val Leu His Pro Leu Met
565 570 575

Ile Leu Asp Leu Leu
580

<210> 3

<211> 555

<212> PRT

<213> Brevibacterium lactofermentum

<400> 3

Val Ser Phe Val Glu Phe His Asn Leu Asn Phe Cys Leu Asn Ser Phe
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Arg His His Pro Arg Ala Ala Ser Glu Leu Leu Thr Pro Arg Asn Leu
20 25 30

Trp Arg Arg Glu Asn His Gly Asn His Val Ala Gly Pro His Gln Thr
35 40 45

Tyr Arg Trp His Pro Gln Gly Leu Cys Gln Gly Val Pro Ala His Ala
50 55 60

Val Gly Glu Gln Ala Ile Ala Ala Ile Gly Leu Asp Ser Ser Ser Leu
65 70 75 80

Pro Thr Ser Asp Ala Ile Phe Ala Ala Val Pro Gly Thr Arg Thr His
85 90 95

Gly Ala Gln Phe Ala Gly Thr Asp Asn Ala Ala Lys Ala Val Ala Ile
100 105 110

Leu Thr Asp Ala Ala Gly Leu Glu Val Leu Asn Glu Ala Gly Glu Thr
115 120 125

Arg Pro Ile Ile Val Val Asp Asp Val Arg Ala Val Leu Gly Ala Ala
130 135 140

Ser Ser Ser Ile Tyr Gly Asp Pro Ser Lys Asp Phe Thr Leu Ile Gly
145 150 155 160

Val Thr Gly Thr Ser Gly Lys Thr Thr Thr Ser Tyr Leu Leu Glu Lys
165 170 175

Gly Leu Met Glu Ala Gly His Lys Val Gly Leu Ile Gly Thr Thr Gly
180 185 190

Thr Arg Ile Asp Gly Glu Glu Val Pro Thr Lys Leu Thr Thr Pro Glu
195 200 205

Ala Pro Thr Leu Gln Ala Leu Phe Ala Arg Met Arg Asp His Gly Val
210 215 220

Thr His Val Val Met Glu Val Ser Ser His Ala Leu Ser Leu Gly Arg

225		230		235		240									
Val	Ala	Gly	Ser	His	Phe	Asp	Val	Ala	Ala	Phe	Thr	Asn	Leu	Ser	Gln
				245					250					255	
Asp	His	Leu	Asp	Phe	His	Pro	Thr	Met	Asp	Asp	Tyr	Phe	Asp	Ala	Lys
			260					265					270		
Ala	Leu	Phe	Phe	Arg	Ala	Asp	Ser	Pro	Leu	Val	Ala	Asp	Lys	Gln	Val
		275					280					285			
Val	Cys	Val	Asp	Asp	Ser	Trp	Gly	Gln	Arg	Met	Ala	Ser	Val	Ala	Ala
	290					295					300				
Asp	Val	Gln	Thr	Val	Ser	Thr	Leu	Gly	Gln	Glu	Ala	Asp	Phe	Ser	Ala
305					310					315					320
Thr	Asp	Ile	Asn	Val	Ser	Asp	Ser	Gly	Ala	Gln	Ser	Phe	Lys	Ile	Asn
			325						330					335	
Ala	Pro	Ser	Asn	Gln	Ser	Tyr	Gln	Val	Glu	Leu	Ala	Leu	Pro	Gly	Ala
			340					345					350		
Phe	Asn	Val	Ala	Asn	Ala	Thr	Leu	Ala	Phe	Ala	Ala	Ala	Ala	Pro	Trp
		355					360					365			
Val	Leu	Met	Ala	Thr	Phe	Ala	Arg	Gly	Met	Ser	Lys	Val	Ala	Val	Pro
	370					375					380				
Gly	Arg	Met	Glu	Arg	Ile	Asp	Glu	Gly	Gln	Asp	Phe	Leu	Ala	Val	Val
385					390					395					400
Asp	Tyr	Ala	His	Lys	Pro	Ala	Ala	Val	Ala	Ala	Val	Leu	Asp	Thr	Leu
				405					410					415	
Arg	Thr	Gln	Ile	Asp	Gly	Arg	Leu	Gly	Ser	Gly	Tyr	Arg	Cys	Trp	Trp
			420					425					430		
Arg	Arg	Asp	Ser	Thr	Lys	Arg	Gly	Pro	Met	Gly	Ser	Cys	Pro	His	Arg
		435					440					445			
Ser	Gly	Ser	Ser	Tyr	Cys	Thr	Asp	Ala	Asn	Leu	Val	Arg	Val	Ala	Gly
	450					455					460				

Thr Ile Arg Ala Ala Val Thr Ala Gly Ala Gln Gln Gly Ala Ser Glu
465 470 475 480

Ser Glu Arg Pro Val Glu Val Leu Glu Ile Gly Asp Arg Ala Glu Ala
485 490 495

Ile Arg Val Leu Val Glu Trp Ala Gln Pro Gly Asp Gly Ile Val Val
500 505 510

Ala Gly Lys Gly His Glu Val Gly Gln Leu Val Ala Gly Val Thr His
515 520 525

His Phe Asp Asp Arg Glu Glu Gly Arg Ala Ala Leu Thr Glu Lys Leu
530 535 540

Asn Asn Lys Leu Pro Leu Thr Thr Glu Glu Gly
545 550 555

<210> 4

<211> 293

<212> PRT

<213> Brevibacterium lactofermentum

Eny.
<400> 4

Met Ile Thr Met Thr Leu Gly Glu Ile Ala Asp Ile Val Gly Gly Arg
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Leu Thr Gly Gly Ala Gln Glu Asp Thr Leu Val Ser Ser Ser Val Glu
20 25 30

Phe Asp Ser Arg Ser Leu Thr Pro Gly Gly Leu Phe Leu Ala Leu Pro
35 40 45

Gly Ala Arg Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys
50 55 60

Gly Ala Val Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile
65 70 75 80

Val Val Pro Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala
85 90 95

His Glu Pro Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg
100 105 110

Leu Ala Arg His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn
115 120 125

Val Val Ala Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe
130 135 140

Ile Ala Thr Val Leu Gly Gln Asp Gly Pro Thr Val Ala Pro Pro Gly
145 150 155 160

Ser Phe Asn Asn Glu Leu Gly Leu Pro His Thr Val Arg Cys Thr Thr
165 170 175

Asp Thr Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His
180 185 190

Ile Lys His Leu Thr Glu Ile Arg Pro Pro Arg Ile Ala Ala Val Leu
195 200 205

Asn Val Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile
210 215 220

Ala Gln Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr
225 230 235 240

B1
can Gly Gly Val Ala Val Leu Asn Ala Asp Asp Pro Phe Val Ala Arg Met
245 250 255

Ala Pro Arg Thr Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala Gly
260 265 270

Gln Ala Lys Lys Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp Ala
275 280 285

Val Ala Arg Ala Ser
290

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Description of Artificial Sequence: synthetic DNA

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gcgcggaattc cgcaacctcg tcgtgacatg

30

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Description of Artificial Sequence: synthetic DNA

<400> 6

gcgcggaattc aagaccaata gccgcgattg cttg

34

B'
cord.